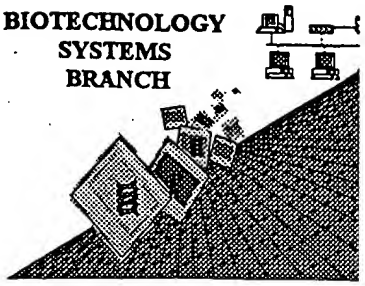
M Tarcha

RAW SEQUENCE LISTING ERROR REPORT

RECEIVED
MAY 30 2000
TECH CENTER 1600/2900

BIOTECHNOLOGY SYSTEMS BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

#6

Application Serial Number: 09/253,153

Art Unit / Team No. : 1627

Date Processed by STIC: 5/15/2000

THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,

2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEI WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

MARK SPENCER 703-308-4212

M. GARCIA

1627

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/253,153

DATE: 05/15/2000
TIME: 12:31:02

Does Not Comply
Corrected Diskette Needed

Input Set : A:\Schwabal.app
Output Set: N:\CRF3\05152000\I253153.raw

```
  3 <110> APPLICANT: Schwabacher, Alan W.
  5 <120> TITLE OF INVENTION: One-Dimensional Compound Arrays and a Method for
  6       Assaying Them
  8 <130> FILE REFERENCE: Schwabacher-One-Dimensional Arrays
 10 <140> CURRENT APPLICATION NUMBER: 09/253,153
 11 <141> CURRENT FILING DATE: 1999-02-19
 13 <150> PRIOR APPLICATION NUMBER: 60/075,629
 14 <151> PRIOR FILING DATE: 1998-02-21
 16 <160> NUMBER OF SEQ ID NOS: 3
 18 <170> SOFTWARE: PatentIn Ver. 2.1
 20 <210> SEQ ID NO: 1
 21 <211> LENGTH: 7
 22 <212> TYPE: PRT
 23 <213> ORGANISM: Artificial Sequence
 25 <220> FEATURE:
 26 <223> OTHER INFORMATION: Description of Artificial Sequence:Sequence of
 27       amino acids synthesized on string
 29 <400> SEQUENCE: 1
 30 His Pro Gln Phe Ala Ala Ala
 31   1               5
 34 <210> SEQ ID NO: 2
 35 <211> LENGTH: 8
 36 <212> TYPE: PRT
 37 <213> ORGANISM: Artificial Sequence
 39 <220> FEATURE:
 40 <223> OTHER INFORMATION: Description of Artificial Sequence: Peptide
 41       synthesized on string
 43 <400> SEQUENCE: 2
W--> 44 Xaa Xaa Pro Gln Phe Ala Ala Ala
 45   1               5
 48 <210> SEQ ID NO: 3
 49 <211> LENGTH: 8
 50 <212> TYPE: PRT
 51 <213> ORGANISM: Artificial Sequence
 53 <220> FEATURE:
 54 <223> OTHER INFORMATION: Description of Artificial Sequence: Peptide
 55       synthesized on string
 57 <400> SEQUENCE: 3
W--> 58 Xaa His Pro Gln Phe Ala Ala Ala
 59   1               5
```

all item 10 on Error Summary Sheet

Item 10

VERIFICATION SUMMARY DATE: 05/15/2000
PATENT APPLICATION: US/09/253,153 TIME: 12:31:03

Input Set : A:\Schwabal.app
Output Set: N:\CRF3\05152000\I253153.raw

L:44 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:44 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:44 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:2
L:58 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:3
L:58 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:3
L:58 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:3

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 09/253,153

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

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1 ____ Wrapped Nucleics
The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 ____ Wrapped Aminos
The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 ____ Incorrect Line Length
The rules require that a line not exceed 72 characters in length. This includes spaces.

4 ____ Misaligned Amino Acid Numbering
The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 ____ Non-ASCII
This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 ____ Variable Length
Sequence(s) ____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.

7 ____ PatentIn ver. 2.0 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence.

8 ____ Skipped Sequences (OLD RULES)
Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 ____ Skipped Sequences (NEW RULES)
Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10 ____ Use of **n**'s or **Xaa**'s (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.

11 ____ Use of <213>Organism (NEW RULES)
Sequence(s) _____ are missing this mandatory field or its response.

12 ____ Use of <220>Feature (NEW RULES)
Sequence(s) ____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)

13 ____ PatentIn ver. 2.0 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.